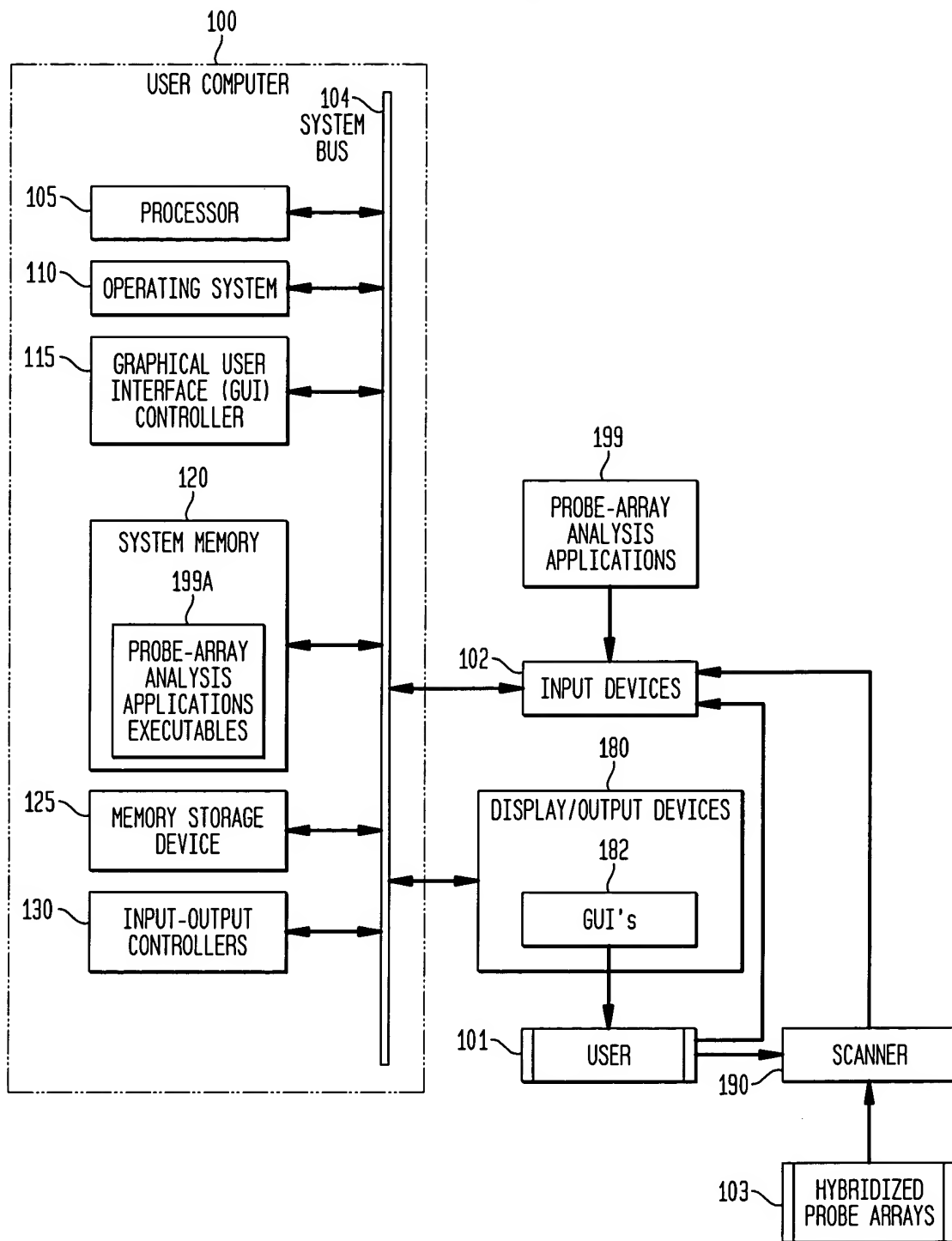


FIG. 1



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FIG. 2

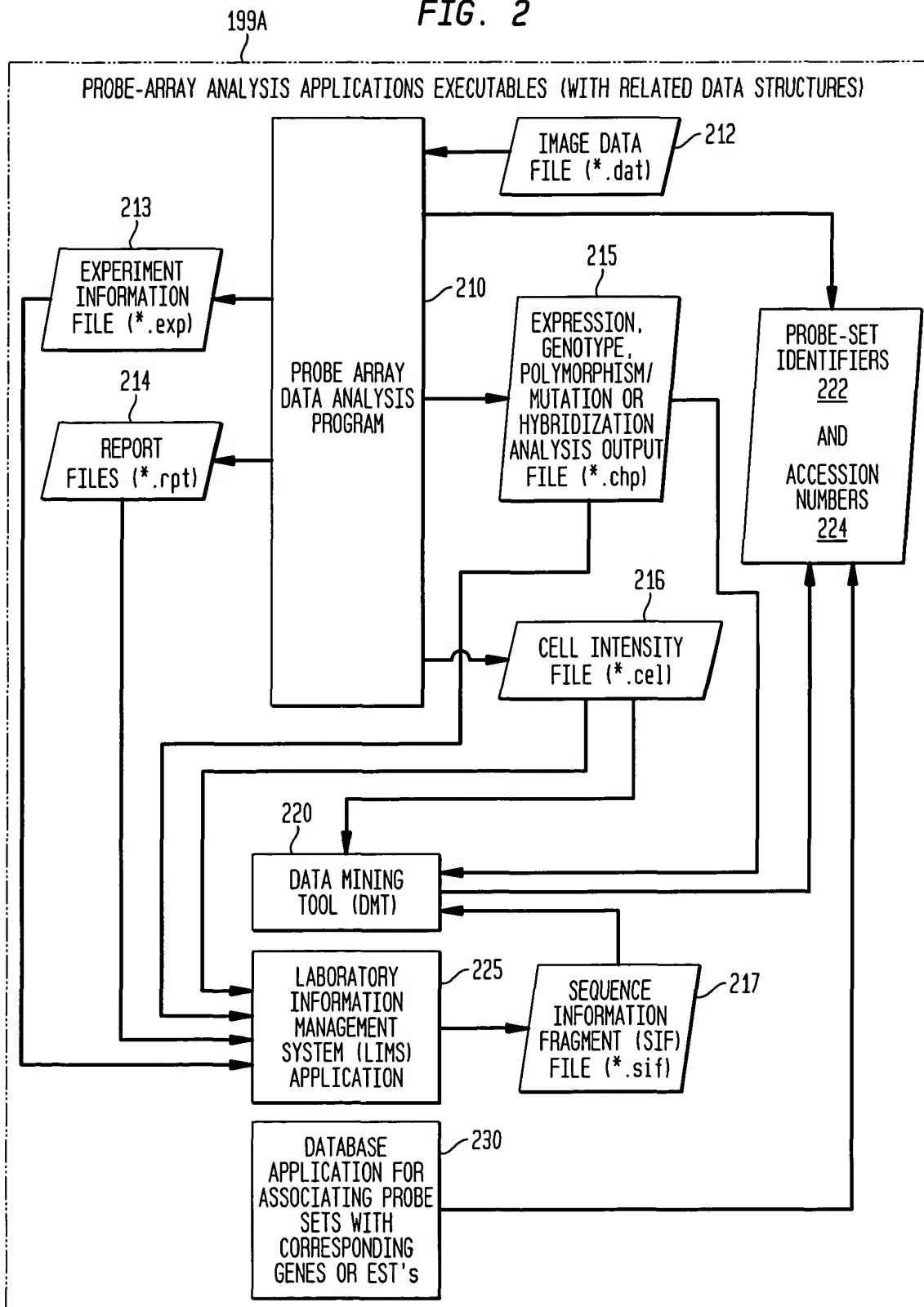
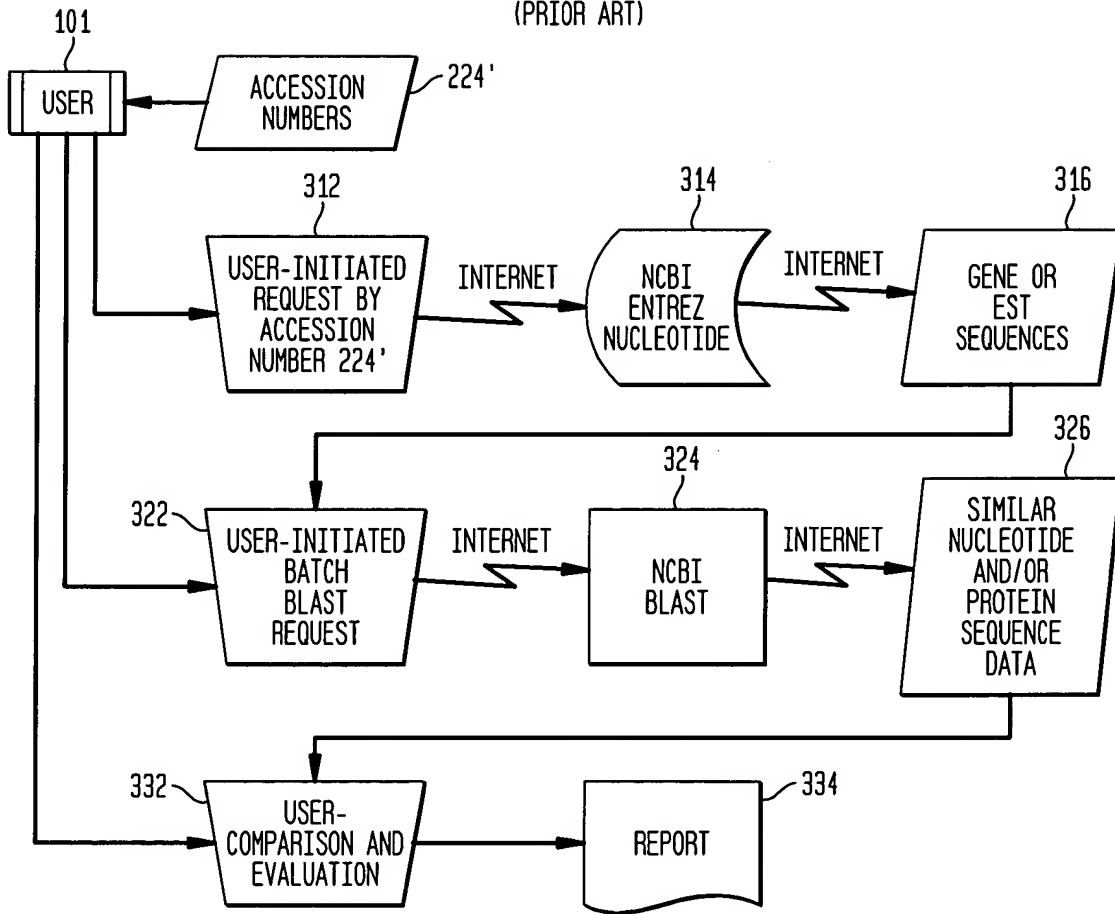
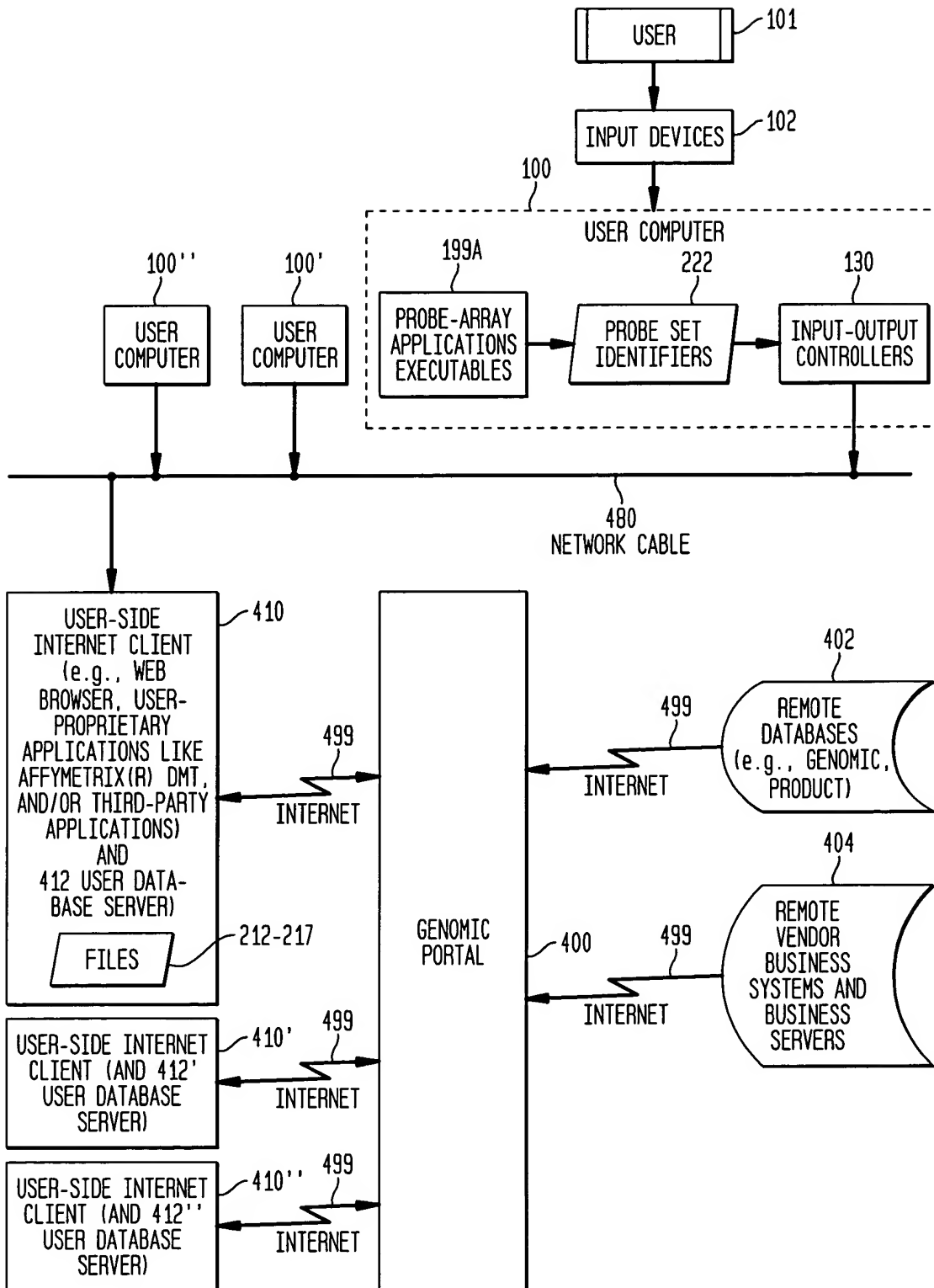


FIG. 3
(PRIOR ART)



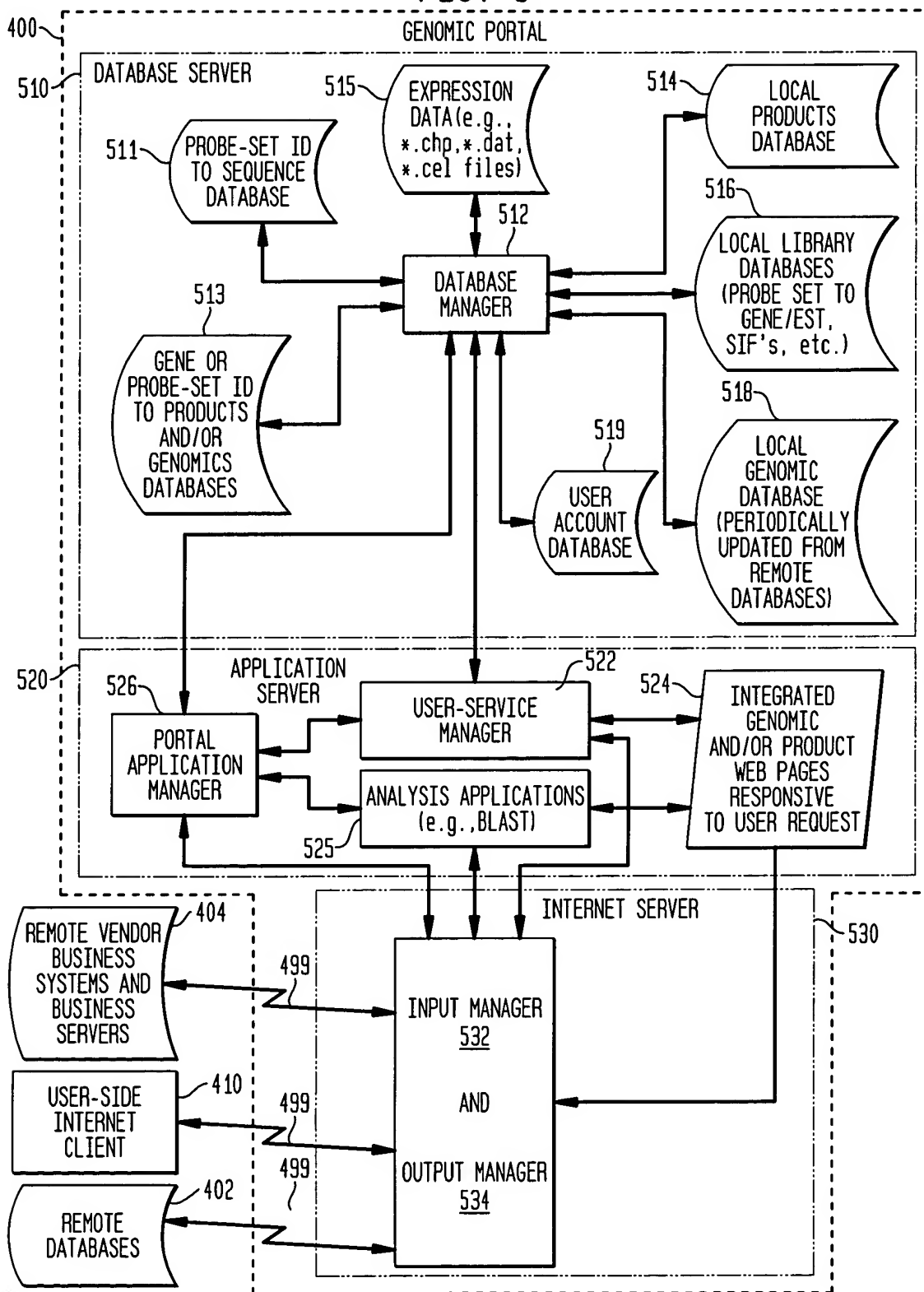
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FIG. 4

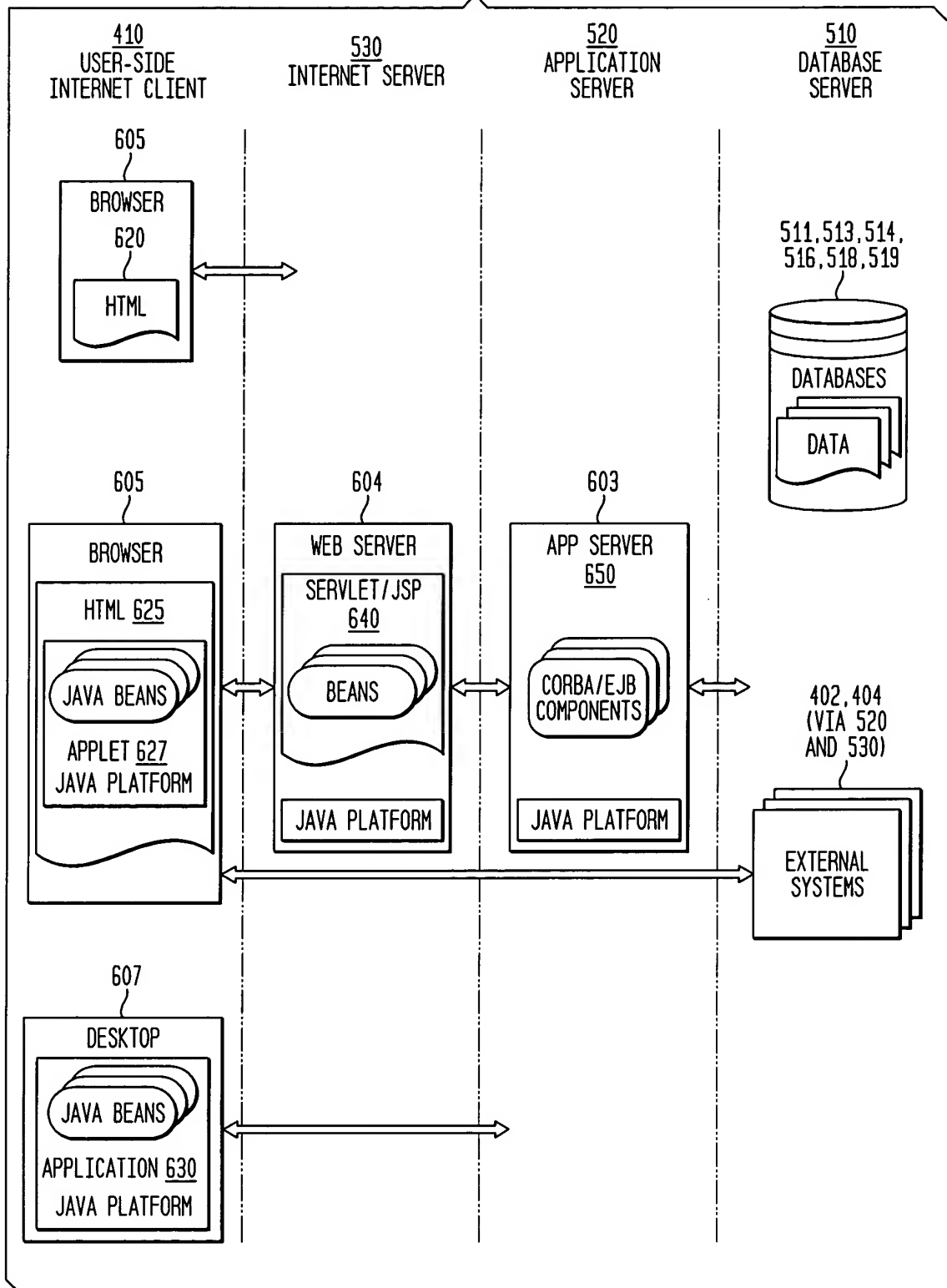


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FIG. 5

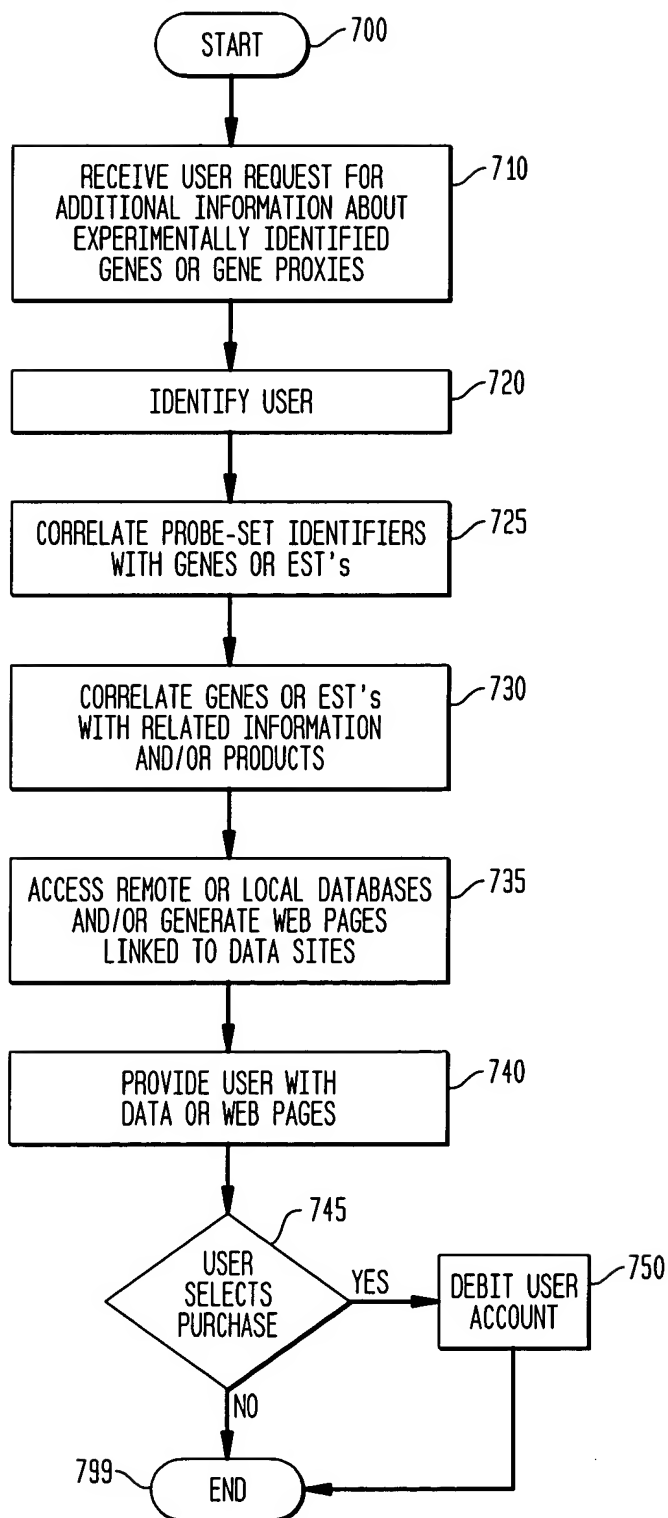


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FIG. 6



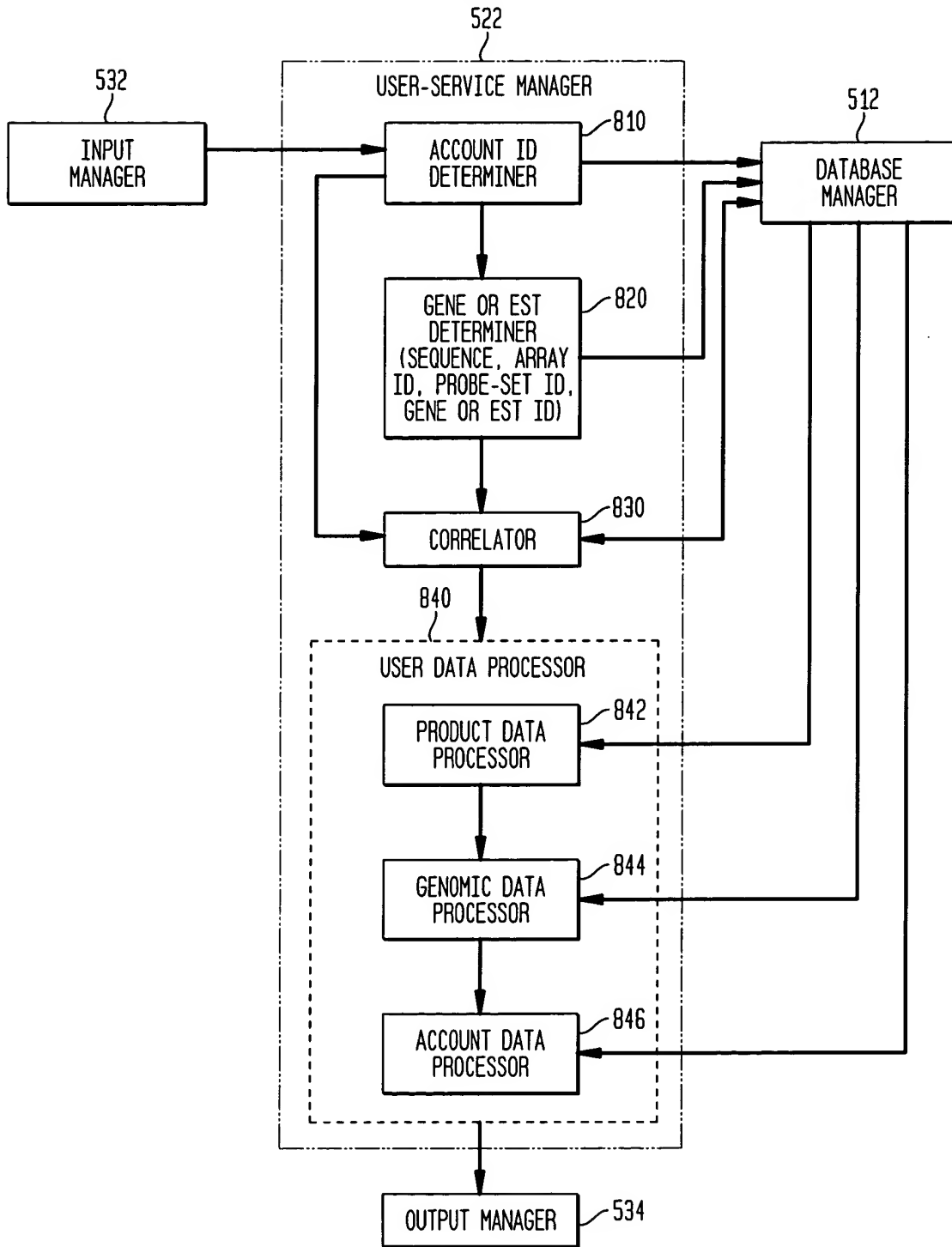


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FIG. 7



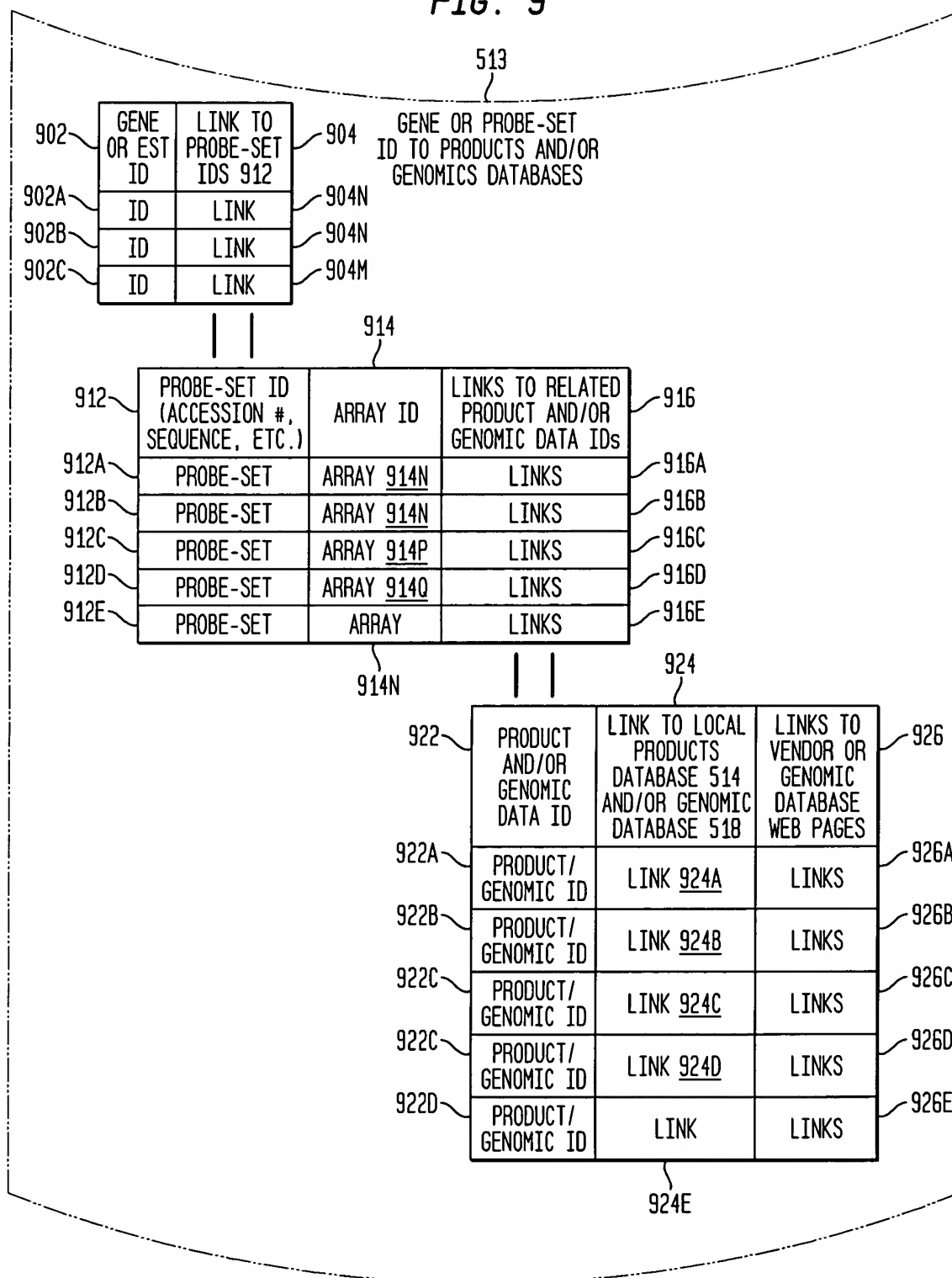
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FIG. 8

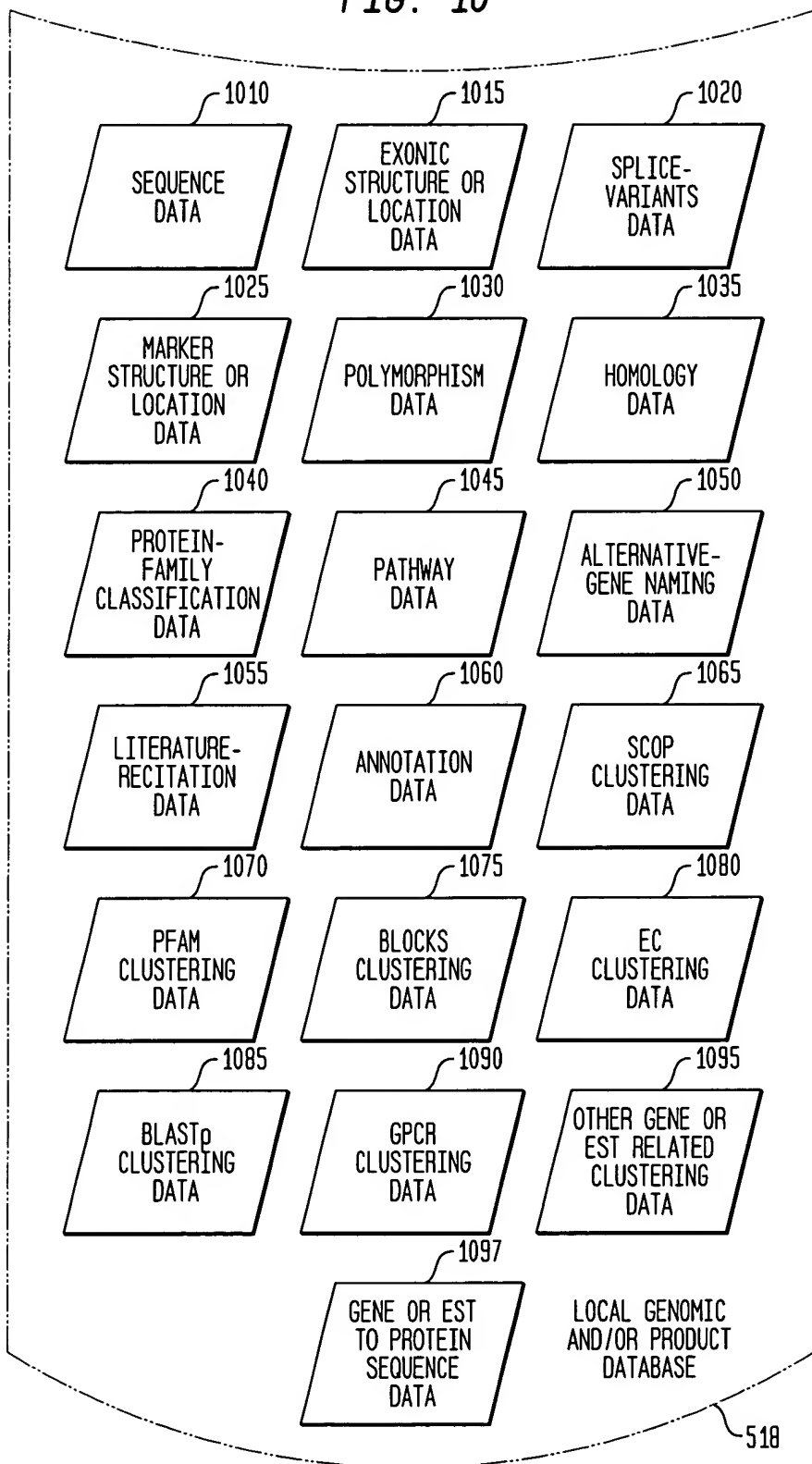


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FIG. 9

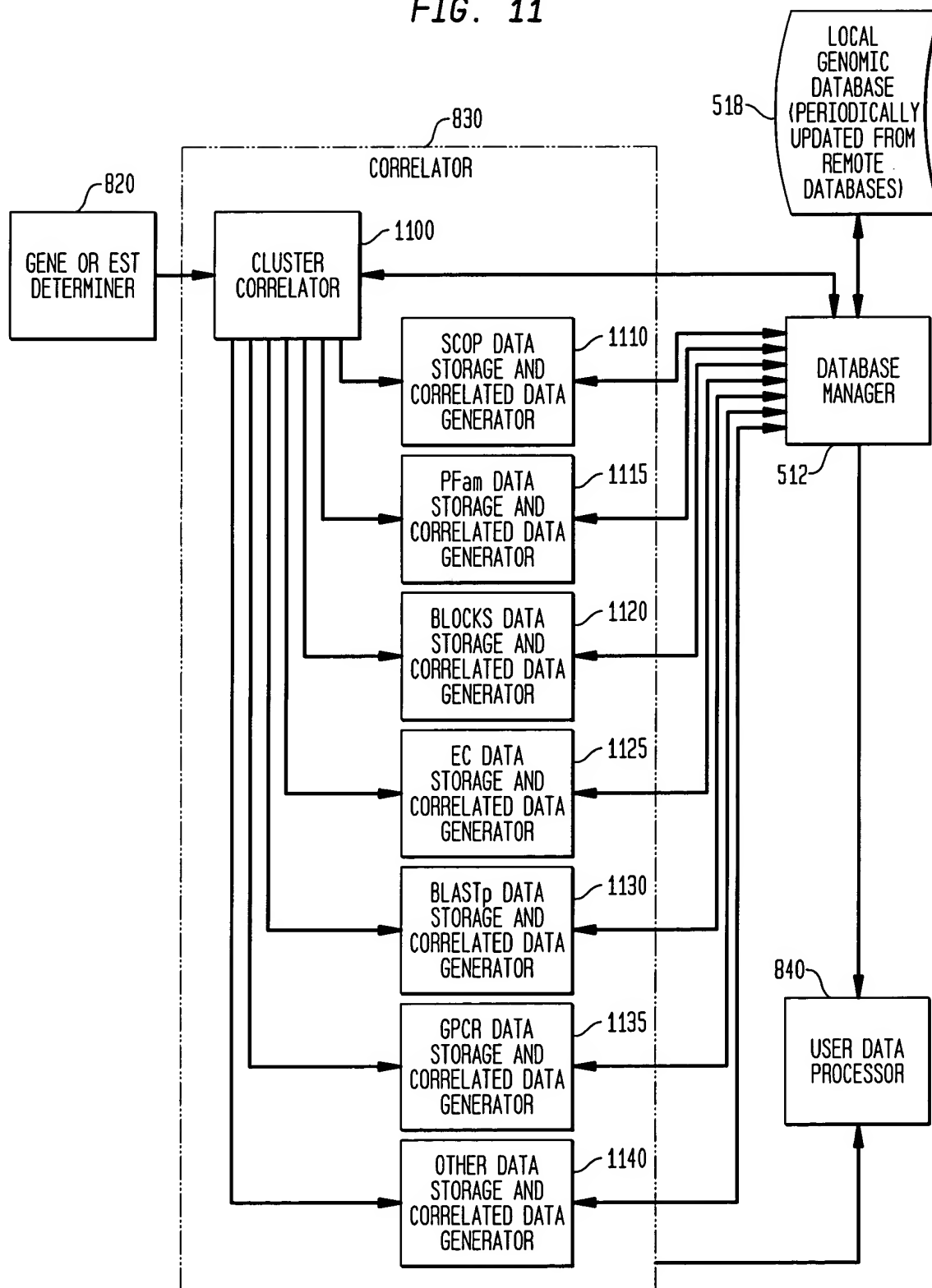


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FIG. 10



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FIG. 11





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FIG. 12

PROTEIN IDENTIFIER 1240

GUI 1200

CLUSTER METHOD IDENTIFIER 1210

RETURNED FAMILY DATA 1220

Domains_PFAM_Hs:NP_003828

ID NP_003828

SEARCH_METHOD hmmpfam

HIT_NAME FBPase WUSTL

HIT_DESC Fructose-1-6-bisphosphatase

OVERALL_EXPECT 1.5e-179 LOG10-179

SIMSPAN Query 12 _ 335 Target 1 _ 342; EXPECT 1.5e-179 LOG10 - 179;

ALIGNMENT

FBPase: domain 1 of 1, from 12 to 335: score 609.9, E = 1.5e-179

*->iTLtrfileeqgedalaKNEatgeltldlssLalaakeiartIarag

+TLtr ++e+ g+ a+ tgelt+ll+s +a k+i+++++ag

NP_003828 12 LTLTRYVMEK-GRQAK---GTGELTQLLSMLTAIKAISSAVRKAG

53

LanllGlagatNsqGDeQKkLDViaddifinAlkasgvvavlaSEEdel

La+l+G+ag++N++GDe+KkLDV+++ ++in+L++s ++vl+SEE++++

NP_003828 54 LAHLYGIAGSVNVTGDEVKKLDVLSNSLVINMLQSSYSTCVLVSEENKDA

103

//

1230

RETURNED ALIGNMENT DATA